

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 7, 2005, 07:04:17; Search time 31.7679 Seconds
(without alignments)
1193.323 Million cell updates/sec

Title: US-09-939-537-29_COPY_1_394
Perfect score: 2029
Sequence: 1 MNRGVPFRHLVLQALALP.....SGQVLESNIKVLPTWSTPV 394

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79: *
2: PIR1: *
3: PIR2: *
4: PIR3: *
5: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2015	99.3	458	1 RWHUT4	T-cell surface gly
2	1867	92.0	432	1 RWCQT4	T-cell surface gly
3	1729	85.2	432	1 RWCQT4	T-cell surface gly
4	1146	56.5	459	2 A46254	CD4 precursor - ra
5	1099	54.2	432	2 S30193	T-cell surface gly
6	989	49.2	457	1 A27449	T-cell surface gly
7	993	48.9	457	1 RWMST4	T-cell surface gly
8	357	17.6	71	2 I60082	CD4 receptor - hum
9	305.5	15.1	99	2 S21461	T-cell surface gly
10	280.5	13.8	99	2 S21462	T-cell surface gly
11	162	8.0	739	2 JS0675	vascular cell adhe
12	155.5	7.7	538	2 JC2457	vascular cell adhe
13	155	7.6	739	2 A41288	vascular cell adhe
14	144	7.1	739	2 UN0581	vascular cell adhe
15	143	7.0	739	2 B41288	vascular cell adhe
16	138	6.8	398	2 I49443	gene 2B4 protein -
17	135	6.7	1259	2 S36126	neural cell adhesi
18	134.5	6.6	1260	1 S05479	neural cell adhesi
19	132	6.5	1011	2 T13669	neutrophil - fr
20	131.5	6.5	6831	2 A88852	protein unc-22 (im
21	131.5	6.5	6839	2 S57242	switchin (similari
22	131.5	6.5	7160	2 T27935	hypothetical prote
23	130.5	6.4	304	2 S04633	myosin-light-chain
24	130	6.4	1906	2 S68335	T-cell receptor ga
25	128	6.3	2783	2 T34416	hypothetical prote
26	127	6.3	2629	2 T32735	telomerase-associ
27	125.5	6.2	725	1 IJMSNG	neural cell adhesi
28	125	6.2	1447	2 A54100	tumor suppressor p
29	125	6.2	1896	2 T08851	Down syndrome cell

30	125	6.2	5175	2 T20992	hypothetical prote
31	125	6.2	5198	2 T43290	hemiscient precurs
32	124	6.1	1115	1 IJMSNL	neural cell adhesi
33	124	6.1	7962	2 I38346	elastic titin - hu
34	123.5	6.1	323	2 S01895	T-cell receptor ga
35	123	6.1	4162	2 T42633	connectin/titin
36	122.5	6.0	761	1 IJHUNG	neural cell adhesi
37	122.5	6.0	1257	1 A41060	neural cell adhesi
38	121.5	6.0	338	2 JC4776	limbic-system-asso
39	121	6.0	946	2 S28061	SCP1 protein - rat
40	121	6.0	1091	1 IJCHNL	neural cell adhesi
41	121	6.0	1427	2 I51669	tumor suppressor -
42	120.5	5.9	333	2 A31923	amalgam protein pr
43	119.5	5.9	702	2 A36319	carcinoembryonic a
44	119	5.9	584	2 T06678	hypothetical prote
45	117	5.8	858	1 IJRTNC	neural cell adhesi

ALIGNMENTS

RESULT 1
RWHUT4
T-cell surface glycoprotein CD4 precursor [validated] - human
N/Alternate names: T-cell surface antigen T4/Les 3
C/Species: Homo sapiens (man)
C/Date: 28-May-1986 #sequence revision 31-Dec-1988 #text change 09-Jul-2004
C/Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039
R/Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, R.
Cell 42, 93-104, 1985
A/Title: The isolation and nucleotide sequence of a cDNA encoding the T cell surface prot
A/Reference number: A90872; NCBI:85254948; PMID:2990730
A/Accession: A90872
A/Molecule type: mRNA
A/Residues: 1-25, 'N', 27-458 <MAD>
A/Cross-references: UNIPROT: P01730
A/Experimental source: clone PT4B
R/Littman, D.R.; Maddon, P.J.; Axel, R.
Cell 55, 541, 1988
A/Title: Corrected CD4 sequence.
A/Reference number: A90907; NCBI:89028665; PMID:3263213
A/Content: annotation; revision to residue 26
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A/Title: CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; NCBI:90182664; PMID:2107024
A/Accession: A32722
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 26-426, 428-458 <CAM>
R/Carr, S.A.; Henling, M.B.; Polena-Wasserman, G.; Sweet, R.W.; Anumula, K.; Barr, J.R.;
J. Biol. Chem. 264, 21286-21295, 1989
A/Title: Protein and carbohydrate structural analysis of a recombinant soluble CD4 recept
A/Reference number: A34194; NCBI:90078232; PMID:2592374
A/Content: disulfide bonds; carbohydrate-binding sites
A/Accession: A34194
A/Molecule type: protein
A/Residues: 26-394 <CAR>
R/Lederman, S.; DeMartino, J.A.; Daugherty, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary, A.
Mol. Immunol. 28, 1171-1181, 1991
A/Title: A single amino acid substitution in a common African allele of the CD4 molecule
A/Reference number: A53287; NCBI:92072555; PMID:1961196
A/Accession: A53287
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 250-264, 'W', 266-280 <LED>
R/Note: sequence extracted from NCBI backbone (NCBI:68249)
R/Bwards, M.C.; Gibbs, R.A.
Genomics 14, 590-597, 1992
A/Title: A human dimorphism resulting from loss of an Alu.
A/Reference number: I54176; NCBI:93052387; PMID:1330888
A/Accession: I54176
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Reference number: A32722; MUID:90182664; PMID:2107024
A/Accession: B32722
A/Molecule type: mRNA
A/Residues: 1-432 <CAM>
A/Cross-references: UNIPROT:P16004; GB:M31135
A/Title: Cloning and sequence of primate CD4 molecules: diversity of the cellular receptor
A/Reference number: A46534; MUID:93049640; PMID:1425921
A/Accession: A46534
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 3-399 <ROM>
A/Note: sequence extracted from NCBI backbone (NCBIP:118332)
C/Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells
C/Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C/Keywords: duplication; glycoprotein; T-cell; transmembrane protein
F:1-432/Product: T-cell surface glycoprotein CD4 #status predicted <EXT>
F:1-371/Domain: extracellular #status predicted <EXT>
F:8-86/Domain: immunoglobulin homology <IM1>
F:111-161/Domain: immunoglobulin homology #status atypical <IM2>
F:191-274/Domain: immunoglobulin homology <IM3>
F:296-347/Domain: immunoglobulin homology <IM4>
F:372-395/Domain: transmembrane #status predicted <TM>
F:396-432/Domain: intracellular #status predicted <INT>
F:16-84,130-159,303-345/Dissulfide bonds: #status predicted
F:271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:296,325/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.3%; Score 2015; DB 1; Length 458;
Best Local Similarity 99.5%; Pred. No. 9.5e-130;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVFRLHLVLAALPAATQGNKVVVGKKGTVELTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVFRLHLVLAALPAATQGNKVVVGKKGTVELTCTASQKKSIOFHMKNNOIK 60
QY 61 IIGNOSFLLTKGSKNDRASSRLMDQGNPFLIKNKIENSDPYICEVEQKEEYVL 120
DB 61 IIGNOSFLLTKGSKNDRASSRLMDQGNPFLIKNKIENSDPYICEVEQKEEYVL 120
QY 121 LVFGLTANSDTHLQGSITLTLSPGSSPVQCSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSDTHLQGSITLTLSPGSSPVQCSPRGKNIQGGKTLVSQLELQDSG 180
QY 121 LVFGLTANSDTHLQGSITLTLSPGSSPVQCSPRGKNIQGGKTLVSQLELQDSG 180
DB 121 LVFGLTANSDTHLQGSITLTLSPGSSPVQCSPRGKNIQGGKTLVSQLELQDSG 180
QY 181 TWTCTVLQNKKEFKIDIVLAFOKASSIVYKKEGEVFPFLAFVTEKLTGSGELMW 240
DB 181 TWTCTVLQNKKEFKIDIVLAFOKASSIVYKKEGEVFPFLAFVTEKLTGSGELMW 240
QY 241 QKERASSKSWITPDLKKNKESVYKRVTPDKLQMGKKLPLHLTLPALPOYAGSGNLTLA 300
DB 241 QKERASSKSWITPDLKKNKESVYKRVTPDKLQMGKKLPLHLTLPALPOYAGSGNLTLA 300
QY 301 LEAKTGKLEQEVNLVVRATOLQKNLTCEVWGFTSPKMLSLKLENKAKVSKREKPVV 360
DB 301 LEAKTGKLEQEVNLVVRATOLQKNLTCEVWGFTSPKMLSLKLENKAKVSKREKPVV 360
QY 361 LNPBAGMOCILSDSGQVLLSESTIKLPTWSTPV 394
DB 361 LNPBAGMOCILSDSGQVLLSESTIKLPTWSTPV 394

RESULT 2
RMC274
T-cell surface glycoprotein CD4 - chimpanzee
N/Alternate names: T-cell surface antigen T4/Len 3
C/Species: Pan troglodytes (chimpanzee)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B32722; A46534
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990

A/Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; MUID:90182664; PMID:2107024
A/Accession: B32722
A/Molecule type: mRNA
A/Residues: 1-432 <CAM>
A/Cross-references: UNIPROT:P16004; GB:M31135
A/Title: Cloning and sequence of primate CD4 molecules: diversity of the cellular receptor
A/Reference number: A46534; MUID:93049640; PMID:1425921
A/Accession: A46534
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 3-399 <ROM>
A/Note: sequence extracted from NCBI backbone (NCBIP:118332)
C/Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells
C/Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C/Keywords: duplication; glycoprotein; T-cell; transmembrane protein
F:1-432/Product: T-cell surface glycoprotein CD4 #status predicted <EXT>
F:1-371/Domain: extracellular #status predicted <EXT>
F:8-86/Domain: immunoglobulin homology <IM1>
F:111-161/Domain: immunoglobulin homology #status atypical <IM2>
F:191-274/Domain: immunoglobulin homology <IM3>
F:296-347/Domain: immunoglobulin homology <IM4>
F:372-395/Domain: transmembrane #status predicted <TM>
F:396-432/Domain: intracellular #status predicted <INT>
F:16-84,130-159,303-345/Dissulfide bonds: #status predicted
F:271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:296,325/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 92.0%; Score 1867; DB 1; Length 432;
Best Local Similarity 98.6%; Pred. No. 1e-119;
Matches 363; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 27 KYVLKKGDTVELTCTASQKKSIOFHMKNNOIKIIGNOSFLLTKGSKNDRASSRL 86
DB 2 KYVLKKGDTVELTCTASQKKSIOFHMKNNOIKIIGNOSFLLTKGSKNDRASSRL 86
QY 87 MDQGNPFLIKNKIENSDPYICEVEQKEEYVLVFGITANSDTHLQGSITLTLSP 146
DB 87 MDQGNPFLIKNKIENSDPYICEVEQKEEYVLVFGITANSDTHLQGSITLTLSP 146
QY 147 PGSSPSVQCSPRGKNIQGGKTLVSQLELQDSGVTCTVLQNKKEFKIDIVLAFOK 206
DB 147 PGSSPSVQCSPRGKNIQGGKTLVSQLELQDSGVTCTVLQNKKEFKIDIVLAFOK 206
QY 207 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSKSWITPDLKKNKESVYK 266
DB 207 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSKSWITPDLKKNKESVYK 266
QY 267 TODPKLQMGKKLPLHLTLPALPOYAGSGNLTLALAKTGKLEQEVNLVVRATOLQKNL 326
DB 267 TODPKLQMGKKLPLHLTLPALPOYAGSGNLTLALAKTGKLEQEVNLVVRATOLQKNL 326
QY 327 TCEVWGFTSPKMLSLKLENKAKVSKREKPVVNLNPEAGMOCILSDSGQVLLSESTIK 386
DB 327 TCEVWGFTSPKMLSLKLENKAKVSKREKPVVNLNPEAGMOCILSDSGQVLLSESTIK 386
QY 387 LPTWSTPV 394
DB 387 LPTWSTPV 394

RESULT 3
RMC274
T-cell surface glycoprotein CD4 - rhesus macaque
N/Alternate names: T-cell surface antigen T4/Len 3
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C/Accession: C32722
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A/Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; MUID:90182664; PMID:2107024

A:Accession: C32722
 A:Molecule type: mRNA
 A:Residues: 1-432 <CAM>
 A:Cross-references: GB:M31134
 C:Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 C:Keywords: duplication; glycoprotein; T-cell; transmembrane protein
 F:1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MNT>
 F:1-371/Domain: extracellular #status predicted <EXT>
 F:9-86/Domain: immunoglobulin homology <IM1>
 F:111-161/Domain: immunoglobulin homology #status atypical <IM2>
 F:180-293/Domain: immunoglobulin homology <IM3>
 F:296-347/Domain: immunoglobulin homology <IM4>
 F:372-395/Domain: transmembrane #status predicted <TM1>
 F:396-432/Domain: intracellular #status predicted <INT>
 F:16-84,130-159,303-345/Disulfide bonds: #status predicted
 F:271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.2%; Score 1729; DB 1; Length 432;
 Best Local Similarity 90.8%; Pred. No. 2,6e-110;
 Matches 334; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 27 KYLVGKGGTVELTCTASQKSIQFHWKNSNQIKIGNOSFLTCKGSPKLNDRADSRRL 86
 DB 2 KYLVGKGGTVELTCTASQKSNQFHWKNSNQIKIGIQGLFLTKGSPKLSBRASRSL 61
 QY 87 WQGNPFLTIKRLKIEDSDTYICEVEDQKEVQLVFGLTANSDFHLQGSGLTLTLESP 146
 DB 62 WQGCSPMTIKRLKIEDSDTYICEVENKEEVELLVFGLTANSDFHLQGSGLTLTLESP 121
 QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTCTVLTQNKKEFKIDIVLAFQK 206
 DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTCTVLTQNKKEFKIDIVLAFQK 181
 QY 207 ASSIYKKEGQVSEFPFLAFVETKLTGSGELMWQERASSKSMITFPLKNEVSVKRV 266
 DB 182 ASSIYKKEGQVSEFPFLAFVETKLTGSGELMWQERASSKSMITFPLKNEVSVKRV 241
 QY 267 TDDPKLQMKKPLPHLTLPOALPOVAGSGLTLTALFAKTKGHQENLVVMAATOLQKRL 326
 DB 242 TDDPKLQMKKPLPHLTLPOALPOVAGSGLTLTALFAKTKGHQENLVVMAATOLQKRL 301
 QY 327 TCEVNGPTSPKMLSLKLENKAKVSKREKPVVNLPEAGMOCILSDSGQVLTLESNIRV 386
 DB 302 TCEVNGPTSPKMLSLKLENKAKVSKREKPVVNLPEAGMOCILSDSGQVLTLESNIRV 361
 QY 387 LPTWSTPV 394
 DB 362 VPTWPTPV 369

RESULT 4
 A46254
 C:Date: 21-Sep-1993 #sequence_cunicleus (domestic rabbit)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 21-Sep-1993 #revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A46254
 R:Hague, B.F.; Sawadiksol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; Kindt, T.J.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
 A:Title: CD4 and its role in infection of rabbit cell lines by human immunodeficiency vi
 A:Reference number: A46254; MUID:92390370; PMID:1518821
 A:Accession: A46254
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-459 <HAG>
 A:Cross-references: UNIPROT:P46630; GB:M92840; NID:g164871; PIDN:AAA3198.1; PID:g164872
 A:Note: sequence extracted from NCBI backbone (NCBI:112732, NCBI:P112733)
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 F:322-372/Domain: immunoglobulin homology <IM1>

Query Match 56.5%; Score 1146; DB 2; Length 459;
 Best Local Similarity 59.9%; Pred. No. 1.4e-70;
 Matches 236; Conservative 64; Mismatches 84; Indels 10; Gaps 5;

QY 1 NNRGVPEFRLTLVLQALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60
 DB 1 NNRRIYFOCLLVLPALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIK 60
 QY 61 ILGNQSGSSSSFWLKNKNSPLSNRVSFKKMMQDQSFPLTKLRLMDSGTGYICEVDKKN 120
 DB 61 ILGNQSGSSSSFWLKNKNSPLSNRVSFKKMMQDQSFPLTKLRLMDSGTGYICEVDKKN 120
 QY 117 EVQLVFGLTANSDFHLQGSGLTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLEL 176
 DB 121 EVQLVFGLTANSDFHLQGSGLTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLEL 180
 QY 177 QDSGTCTV-LQNKKEVFKIDIVLAFQKASSIYKKEGQVSEFPFLAFVETKLTGS 235
 DB 181 QDSGTCTV-LQNKKEVFKIDIVLAFQKASSIYKKEGQVSEFPFLAFVETKLTGS 238
 QY 236 GELMWQERASSKSMITFPLKNEVSVKRVTPDQPKLQMKKPLPHLTLPOALPOVAGSG 295
 DB 239 GELMWQERASSKSMITFPLKNEVSVKRVTPDQPKLQMKKPLPHLTLPOALPOVAGSG 298
 QY 296 NLTLALFAKTKGHQENLVVMAATOLQKRLTCEVNGPTSPKMLSLKLENKAKVSKRE 355
 DB 299 NLTLALFAKTKGHQENLVVMAATOLQKRLTCEVNGPTSPKMLSLKLENKAKVSKRE 355
 QY 356 KPVVNLPEAGMOCILSDSGQVLTLESNIRVPT 389
 DB 356 KPVVNLPEAGMOCILSDSGQVLTLESNIRVPT 389

RESULT 5
 S30193
 T-cell surface glycoprotein CD4 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S30193
 R:Wilde, K.F.; Comer, G.B.; Mintz, D.H.; Alejandro, R.
 Biochim. Biophys. Acta 1172, 315-318, 1993
 A:Title: Primary structure of the canine CD4 antigen.
 A:Reference number: S30193; MUID:93192324; PMID:7916632
 A:Accession: S30193
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-432 <MLT>
 A:Cross-references: EMBL:X68865; NID:g288652; PIDN:CA37664.1; PID:g4467377
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 C:Keywords: glycoprotein
 F:202-311/Domain: immunoglobulin homology <IM1>

Query Match 54.2%; Score 1099; DB 2; Length 432;
 Best Local Similarity 57.7%; Pred. No. 2e-67; Mismatches 86; Indels 18; Gaps 6;
 Matches 226; Conservative 62; Mismatches 86; Indels 18; Gaps 6;

QY 12 LVLQALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIKIGNOSFLT 71
 DB 1 LVLQALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNQIKIGNOSFLT 71
 QY 72 GPKLNDRADSRRLMDQGNPFLTIKRLKIEDSDTYICEVEDQKEVQLVFGLT- 127
 DB 61 GPKLNDRADSRRLMDQGNPFLTIKRLKIEDSDTYICEVEDQKEVQLVFGLT- 119
 QY 128 -----NSDTHLQGSGLTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLELQDSGT 182
 DB 120 GSSSGSSNIRLQGSGLTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLELQDSGT 179
 QY 183 TCTVLTQNKKEVFKIDIVLAFQKASSIYKKEGQVSEFPFLAFVETKLTGSGELMWQ 242
 DB 180 TCTVLTQNKKEVFKIDIVLAFQKASSIYKKEGQVSEFPFLAFVETKLTGSGELMWQ 237
 QY 243 ERASSKSMITFPLKNEVSVKRVTPDQPKLQMKKPLPHLTLPOALPOVAGSGNTLALF 302
 DB 238 QDASSSLTWISFTLENKRLSKENAHAPKLTQMKESLPFLTPVLVSRVAGSGITLNL- 296

A/Accession: S19872
 A/Molecule type: mRNA
 A/Residues: 1-2, 'G', '4-121, 'HL', 124-165, 'N', 167-738, 'G', <W12>
 A/Cross-references: EMBL:X63722; NID:g57472; PIDD:CAA5254.1; PID:g57472
 R/Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.; Colla
 Biochem. Biophys. Acta 1131, 214-216, 1992
 A/Title: Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.
 A/Reference number: S23136; MUID:92305064; PMID:1377031
 A/Accession: S23136
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-2, 'G', '4-165, 'N', 167-738, 'G', <W12>
 C/Comment: This protein interacts with the beta-1 integrin very late antigen 4 on leuko
 C/Genetics:
 A/Genes: VCAM-1
 C/Keywords: cell adhesion; transmembrane protein
 F1-24/Domain: signal sequence #status predicted <SIG>
 F125-739/Product: vascular cell adhesion molecule 1 #status predicted <VAS>
 F1239-293/Domain: immunoglobulin homology <IMM1>
 F128-385/Domain: immunoglobulin homology <IMM2>
 F1526-581/Domain: immunoglobulin homology <IMM3>
 F1676-696/Domain: transmembrane #status predicted <TRA>
 F1697-715/Domain: intracellular #status predicted <INT>

Query Match 8.0%; Score 162; DB 2; Length 739;
 Best Local Similarity 22.0%; Pred. No. 0.0024;
 Matches 86; Conservative 60; Mismatches 155; Indels 90; Gaps 14;

QY 33 KGDVLTCTAGSKSIQFHMKNSNQIKILGNQSLTGTGPKSLNDRADSRSLMDQNF 92
 DB 238 EGAATVMTGASLEGLPAPRIFFMSK-----LDNGVQLL-----SGNA 274
 QY 93 PLIKNLKIEDSDTYICE---VEDQEEVQLV-----FGLTNSDTHLLQGQSLTLT 142
 DB 275 TLTLAMREDESGIYCEGVNLVGRKTVELIVQKRPVNDISPSQVAAGVDSVULT 334
 QY 143 LESPSSPSVQCRSPRGNIG-----GKTLVSQLELDQSGTWCTVILQNRKVEP 195
 DB 335 CAVGCDSFSPFWRQTDSPLNGEVADGATSTLTLSPGVDEHSHYLCTVTCQRKLEK 394
 QY 196 KIDIVLAQKXASIVYKKEGQVEFSFPLA-----FIVEKLTGSG 236
 DB 395 TLQVEYYSF-----DEDPETIEISGPLVGRPVTVNCTVNVYRPFHLLEIELKGET 445
 QY 237 ELWMOAERAS-SSKSWITFDLKNKEVSVKRVTDPLQMGKTL-----PLHLLPQLP-Q 290
 DB 446 TLNKLREIEIGTS---LETSLSEMTFIPFAD-----TGKALVCLAKLHSSQMESEPRQ 498
 QY 291 VAGSGNLTALBAKTKGLHGVNLVVMRAVTLQKNITCEVWGPTSPKMLSLKLENKAK 350
 DB 499 ROSTQTLVNVVAPKEPTIVWSPPVPEEGSPV--NLTCSDDGFPPTKILMSRQLKNGELQ 556
 QY 351 VGRKRPVAVLNPEAGMOCCLSDSGQVLE 381
 DB 557 PLISQ-----NTTISFMATKMEDSGIYCE 580

RESULT 12

JC2457
 vascular cell adhesion protein - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
 A/Accession: JC2457
 R/Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
 Biochem. Biophys. Res. Commun. 201, 805-812, 1994
 A/Title: Cloning and expression kinetics of porcine vascular cell adhesion molecule.
 A/Reference number: JC2457; MUID:94271236; PMID:7516159
 A/Accession: JC2457
 A/Molecule type: mRNA
 A/Residues: 1-538 <TSA>
 A/Cross-references: UNIPROT:Q28939; EMBL:U08351; NID:g474382; PIDD:AAA21542.1; PID:g4743
 C/Keywords: glycoprotein; transmembrane protein
 F1497-511/Domain: transmembrane #status predicted <TMM>

F175,157,271,330,360/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 7.7%; Score 155.5; DB 2; Length 538;
 Best Local Similarity 23.4%; Pred. No. 0.0045;
 Matches 65; Conservative 49; Mismatches 91; Indels 73; Gaps 11;

QY 32 KKGDVLTCTAGSKSIQFHMKNSNQIKILGNQSLTGTGPKSLNDRADSRSLMDQNF 91
 DB 235 QEGDSMMMTCTSEGLPAPRIISW-----SKLDNDQQLL-----SGN 271
 QY 92 PPLIKNLKIEDSDTYICE---VEDQEEVQLV-----FGLTNSDTHLLQGQSLTL 141
 DB 272 ATLTLAMREDESGIYCEGVNLVGRKTVELIVQKRPVNDISPSQVAAGVDSVULT 331
 QY 142 LESPSSPSV-----QCRSPRGNIGKTLVSQLELDQSGTWCTVILQ-----NQRKV 193
 DB 332 TCSSGPPAPKTLWSEKLDGMLPELSENTVLTSTKMEDSGIYCEGINQAINREV 391
 QY 194 EFKI-----DIVLAQKXAS-----SIYKKE-----GEQVEFSFPLA 226
 DB 392 ELILQAPKDQLTFPSESVEKDPVLIISCTGVNPPVTLILKKKAEKGTIVLKSTDGA 451
 QY 227 FIVEKLT---TSGELWMOAERASSSKSWITFDLQKKE 260
 DB 452 YTIHRARLADAGVCEKSKNEIGQLRS-ITLDVKGRE 488

RESULT 13

A41288
 vascular cell adhesion molecule 1, long splice form precursor - human
 N/Alternate names: VCAM-1
 C/Species: Homo sapiens (man)
 C/Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
 A/Accession: A41288; S11476; A39755; B39755; A61160; A4352; PH1379; A39554
 R/Cybulsky, M.I.; Fries, J.W.U.; Williams, A.J.; Sultan, P.; Eddy, R.; Byers, M.; Shows,
 Proc. Natl. Acad. Sci. U.S.A. 88, 7859-7863, 1991
 A/Title: Gene structure, chromosomal location, and basis for alternative mRNA splicing of
 A/Reference number: A41288; MUID:91352090; PMID:1715583
 A/Accession: A41288
 A/Molecule type: DNA
 A/Residues: 1-739 <CYB>
 A/Cross-references: UNIPROT:P19220; GB:M73255; NID:G340195; PIDD:AAA61270.1; PID:G340196
 R/Polte, T.; Newman, W.; Gopal, T.V.
 Nucleic Acids Res. 18, 5901, 1990
 A/Title: Full length vascular cell adhesion molecule 1 (VCAM-1).
 A/Reference number: S11476; MUID:91016951; PMID:1699207
 A/Accession: S11476
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-739 <POL>
 A/Cross-references: EMBL:X53051; NID:G37648; PIDD:CAA37218.1; PID:G37649
 R/Hessio, C.; Tizard, R.; Vassallo, C.; Schiffer, S.B.; Goff, D.; Moy, P.; Chi-Rosso, G.
 J. Biol. Chem. 266, 6682-6685, 1991
 A/Title: Cloning of an alternate form of vascular cell adhesion molecule-1 (VCAM1).
 A/Reference number: A39755; MUID:91201302; PMID:1707873
 A/Accession: A39755
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 25-646, 648-739 <HES1>
 A/Cross-references: GB:M60335
 A/Note: the complete translation is not shown
 A/Accession: B39755
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-739 <HES2>
 A/Cross-references: GB:M60335; NID:G340193; PIDD:AAA61269.1; PID:G340194
 R/Cybulsky, M.I.; Fries, J.W.U.; Williams, A.J.; Sultan, P.; Davis, V.M.; Gimbrone Jr., P
 Am. J. Pathol. 138, 815-820, 1991
 A/Title: Rapid communication. Alternative splicing of human VCAM-1 in activated vascular
 A/Reference number: A61160; MUID:91189297; PMID:1707234
 A/Accession: A61160
 A/Status: not compared with conceptual translation

A: Molecule type: mRNA
 A: Residues: 25-401, 'T', 403-686 <CY2>
 A: Accession: JN0581
 J. Biol. Chem. 267, 16323-16329, 1992
 A: Title: Characterization of the promoter for vascular cell adhesion molecule-1 (VCAM-1)
 A: Reference number: A43352; MUID:92355594; PMID:1379595
 A: Accession: A43352
 A: Molecule type: DNA
 A: Residues: 1-21 <IAD>
 A: Cross-references: GB:M92431; NID:9340197
 A: Note: Sequence extracted from NCBI backbone (NCBIN:110680, NCBIPI:110681)
 R. Osborn, L.; Vassalli, C.; Benjamin, C.D.
 J. Exp. Med. 176, 99-107, 1992
 A: Title: Activated endothelium binds lymphocytes through a novel binding site in the alpha
 A: Reference number: M1379; MUID:9230860; PMID:1377228
 A: Accession: M1379
 A: Molecule type: protein
 A: Residues: 25-181, 'G', 183-402 <OSB>
 C: Comment: This adhesion molecule is induced on endothelial cells by inflammatory cytokines
 C: Genetics:
 A: Gene: GDB:VCAM1
 A: Cross-references: GDB:127922; OMIM:192225
 A: Map position: 1p32-1p31
 C: Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-739/Product: vascular cell adhesion molecule 1, long splice form #status predicted
 F: 25-698/Domain: extracellular #status predicted <EXT>
 F: 699-720/Domain: transmembrane #status predicted <TM>
 F: 721-735/Domain: intracellular #status predicted <INT>
 F: 273,365,417,463,531,561/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 155; DB 2; Length 739;
 Best Local Similarity 21.9%; Pred. No. 0.0073;
 Matches 91; Conservative 71; Mismatches 166; Indels 88; Gaps 18;

8 RHLLVLTQLALPAAT--OGNRYVLEKKGDTVELTCTASQKSIQPHWKNQIKILNQ 65
 211 RQAVKELQYISPKNTVISVNPSTKLQEGSVTMTCSSEGLPAPEIFW----- 258

66 GSFLLTKGPKKLRADSRSLMDQGNFPIIKLKIEDSDTYICE---VEDQKEVOL 121
 259 -----SKKLIDNGLQHL---SGNATLTLLAMREDSGIYVCEGVNLIGKRKKEVELI 307

122 V----FGLTANSQTHLLQ--GOSLTLTLESPPSSVQCRSPRGNIQ-----GKT 168
 308 VQEKFPYVETISGPRPAAQIGDSWMLTSCVMGCESSFSWRITQIDSPISGKVRSEGTNST 367

169 LSVSOLQDQSGTWTCTVLONQKVEFKIDIVLAFQKASIVYK---KEGROVES--- 222
 368 LTLSPVSPENHSYLTCTVCGHKLEKGLQVELYSFRPDEIEMSGLVNNGSVTVSCKV 427

223 ---PPL-AFTVEKLTGSGELMWOAERASSSKSNTF---DLKNEVSVKRYTODPKLQ- 273
 428 PSVYPLRLLEILKMKETIL-----ENIEFLBDTDMKSLKNSLEMTFPIITID 476

274 MKKKL---PLHLTLPLQALPOYAGSNTLALAEKTKGLHGVNVLVMAATQLOK-----N 325
 477 TKALVLCQAKHIDMEFEPKQROQ---TQTLVNVAP--RDTTVLVASSSILIESSSVN 531

326 LITCEVWGPSPKMLSLKLENKAKVSKREKPVVNLNPEAGMWQCLSSDGVLTLE 381
 532 MTCLSGFPAPKILWROPLNGELQPLSENATITLSTK-----MEBSGVYLCE 580

RESULT 14
 JN0581
 vascular cell adhesion molecule-1 long splice form precursor - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
 C: Accession: JN0581; US0674; A40275; A48919
 R: Araki, M.; Araki, K.; Vassalli, P.
 A: Title: Cloning and sequencing of mouse VCAM-1 cDNA.

A: Reference number: JN0581; MUID:93246254; PMID:7683304
 A: Accession: JN0581
 A: Molecule type: mRNA
 A: Residues: 1-739 <ARA>
 A: Cross-references: UNIPROT:P29533; EMBL:X67783; NID:9298116; PID:CA447989.1; PID:929811
 R: Hession, C.; Moy, P.; Tizad, R.; Chisholm, P.; Williams, C.; Wyse, M.; Burki, L.; Mij
 Biochem. Biophys. Res. Commun. 183, 163-169, 1992
 A: Title: Cloning of murine and rat vascular cell adhesion molecule-1.
 A: Reference number: J50674; MUID:92181437; PMID:1371918
 A: Accession: J50674
 A: Status: nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-739 <HES>
 A: Cross-references: GB:M84487; NID:9202345; PID:AAA40545.1; PID:9202346
 R: Miyake, K.; Medina, K.; Ishihara, K.; Kimoto, M.; Auerbach, R.; Kincaide, P.W.
 J. Cell Biol. 114, 557-565, 1991
 A: Title: A VCAM-like adhesion molecule on murine bone marrow stromal cells mediates bindi
 A: Reference number: A40275; MUID:91317872; PMID:1715592
 A: Accession: A40275
 A: Molecule type: protein
 A: Residues: 'XX', 27-32 <MTY>
 R: Cybulsky, M.I.; Allan-McMamed, M.; Collins, T.
 Genomics 18, 387-391, 1993
 A: Title: Structure of the murine VCAM1 gene.
 A: Reference number: A48919; MUID:94117008; PMID:7507076
 A: Accession: A48919
 A: Molecule type: DNA
 A: Residues: 1-692, 'N', 694-739 <CYB>
 A: Cross-references: GB:L22353; NID:9347981; PID:AAA16921.1; PID:9459893; GB:L22301
 C: Comment: This protein is a transmembrane protein and interacts with the beta-1 integrin
 C: Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-739/Product: vascular cell adhesion protein-1 #status predicted <MAT>
 F: 239-293/Domain: immunoglobulin homology <IMW1>
 F: 328-385/Domain: immunoglobulin homology <IMW2>
 F: 527-581/Domain: immunoglobulin homology <IMW3>
 F: 699-720/Domain: transmembrane #status predicted <TM>
 F: 225,273,424,531,561/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.1%; Score 144; DB 2; Length 739;
 Best Local Similarity 20.2%; Pred. No. 0.041;
 Matches 79; Conservative 65; Mismatches 147; Indels 100; Gaps 15;

32 KKGDTVELTCTASQKSIQPHW--KNSNQI-KILNGSGFLTKGSKLNRADSRSLMD 88
 237 QEGGAVTMTCSSEGLPAPEIFGKRLDNEVOLL----- 270

89 QGNFPIIKLKIEDSDTYICE---VEDQKEVOLV-----FGLTANSQTHLLQSGS 138
 271 SGNATLTLLAMREDSGVVYVCEGVNLIGDKALEVELVQEKFPYVIDISPGSQAQVGD 330

139 LTLTLESPPGSPVQCRSPRGNIQ-----GKTLVSQLELDQSGTWTCTVLONQK 191
 331 VVLTCAIIGCDSPSPSWRTQTPSPNGVVRNAGASTVLSSVGEDEHSYLCAYTCLQR 390

192 KYEFPKIDIVLAFQKASIVYKKEGROVESFPLA-----FTVEK 232
 391 TLEKRIQVEVYF-----PEDPVIMSGPLVHGRPVYVNCVYVNPYPPDHLIEL 441

233 TSGSGLMWOAERASSSKSWI--TFDLKNEVSVKRYTODPKLQ--MGKKL---PLHLTLQ 286
 442 KG-----FTLTKKVVYLEMGIKSLKTLTLETFPIITIDTGLVCLARLHSGEME 493

287 ALPOYAGSNTLALAEKTKGLHGVNVLVMAATQLOK-----NLCEVWGPSPKMLSL 342
 494 SEPKQROQVQPLVNVAP-----KETTIVWSPSPILIESSPVNLCSGDIAPKILW 548

343 KLENKAKVSKREKPVVNLN--PEAGMWQ 370
 549 QLNNGELQPLSENTITLTFTWSTRDSDGIYVC 579

RESULT 15

B41288
vascular cell adhesion molecule 1, short splice form precursor - human
N:Alternate names: VCAM-1
C:Species: Homo sapiens (man)
C>Date: 03-Apr-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C/Accession: B41288; A33758
R:Cybulsky, M.I.; Fries, J.W.U.; Williams, A.U.; Sultan, P.; Eddy, R.; Byers, M.; Shows, Proc. Natl. Acad. Sci. U.S.A. 88, 7859-7863, 1991
A>Title: Gene structure, chromosomal location, and basis for alternative mRNA splicing
A/Reference number: A41288; MUID:91552090; PMID:1715583
A/Accession: B41288
A/Molecule type: DNA
A/Residues: 1-647 <CYB>
A/Cross-references: UNIPROT:P19320; GB:W73255
R:Osborn, L.; Hession, C.; Tizard, R.; Vassallo, C.; Luhnensky, S.; Chi-Rosso, G.; Lobb, Cell 59, 1203-1211, 1989
A>Title: Direct expression cloning of vascular cell adhesion molecule 1, a cytokine-indu
A/Reference number: A33758; MUID:90090619; PMID:2688898
A/Accession: A33758
A/Molecule type: mRNA
A/Residues: 1-647 <OSB>
A/Cross-references: GB:M30257; MUID:9179885; PIDN:AA51917.1; PID:9179886
C/Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-647/Product: vascular cell adhesion molecule 1, short form #status predicted <Mat>
F:25-606/Domain: extracellular #status predicted <EXT>
F:607-628/Domain: transmembrane #status predicted <TM>
F:629-647/Domain: intracellular #status predicted <INT>
F:273,325,371,439,469/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 143; DB 2; Length 647;
Best Local Similarity 20.9%; Pred. No. 0.04;
Matches 105; Conservative 81; Mismatches 151; Indels 166; Gaps 25;

QY 16 LALLPAATGKNV-----VLGKGDYELTCTASQKSIQFMWNSNQIKLG---NQ 65
DB 15 LMIMPAASQAFKLETPESRYLAQIGDSVLTCTGCSPPFSWRTQIDSPINGKVTNE 74
QY 66 G--SFLTKGPKSKLNDK-----ADSRKSLWDOG-----NFP----- 93
DB 75 GTTSTLTNNPVSPFGNHSYLTCTATCESRK--LEKGIQVEIYSPKDPRIHLGPLEAGKP 132
QY 94 -----LIIKNLK-----IEDSD-----TYICEVED--- 113
DB 133 ITVKCSVADVPPDRLEIDLKGDHLKMSQFLEADRSLETSLVFTFTPIEDIGKV 192
QY 114 -----QKEVQLVFG-----LTNSDTHLQGSLLTLTLESPPGS 149
DB 193 IVCRAKLHIDEMDSVPTVQAQAVKELOVYISPKNTVIVSNPSTKLOGSSVTMTCSSEGLP 252
QY 150 SPSV-----QCRSPRGKNIQGGKTLVSQLELQDSGTWTC---TVLQNKQVTEFKIDIV 201
DB 253 ABEIFWMSKLDNGNLQHLSGNATLITLIARMEDSGIYCEGNLIGKMKVE---LIV 308
QY 202 LAFQKASSIIVK---KEGEQVEFS-----FPL-AFTVEKLTGSGELMWQAERASSSKSW 251
DB 309 QAFPRDPRIEMSGGLVNGSSVTWSCVPSEVYPLDRLEIELKGETIL-----EN 357
QY 252 ITF-----DLKNEVSVKRTQDPKQ-MGKKL-----PLHLTPQALPOYAGSGNLTALAE 302
DB 358 IEFLEDTDMKSLKNSLEMTPIPTLEDTKALVCOAKLHIDMEPEPKQRS---TQTLV 414
QY 303 AKTGKIHQEVNIVVMRATQLOK---NLTCVWGPTSPKMLSLKLENKAKVSKREKPV 358
DB 415 VNVAV--RDTTVLVSSSILBEGSSVNMCTLSQFPAPKILMSRQLPNGELOPLSENATL 472
QY 359 WVLNPEAGMGCCLSDSQVLLIE 381
DB 473 TLISTK-----MEDSGVYLCE 488